

# Computational analysis of sc-RNAseq datasets

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Updated date: Jun 27, 2022

 An abbreviated version of this protocol was published in eLIFE in Jan 2021

Defining human mesenchymal and epithelial heterogeneity in response to oral inflammatory disease

DOI: 10.7554/eLife.62810

## Related files

 \_x2A\_eLife-code-upload.txt



**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Caetano, A. , Yianni, V. and Sharpe, P. (2022). Computational analysis of sc-RNAseq datasets. Bio-protocol Preprint. [bio-protocol.org/prep1746](https://bio-protocol.org/prep1746).
2. Caetano, A. J., Yianni, V., Volponi, A., Booth, V., D'Agostino, E. M. and Sharpe, P.(2021). Defining human mesenchymal and epithelial heterogeneity in response to oral inflammatory disease. eLIFE. DOI: [10.7554/eLife.62810](https://doi.org/10.7554/eLife.62810)

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